

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: CAROLYN PETERSEN  
JIN-XING HUANG
- (ii) TITLE OF INVENTION: CRYPTOPAIN VACCINES, ANTIBODIES, PROTEINS,  
PEPTIDES, DNA AND RNAS FOR PROPHYLAXIS,  
TREATMENT, DIAGNOSIS AND  
DETECTION OF  
CRYPTOSPORIDIUM PARVUM
- (iii) NUMBER OF SEQUENCES: 16
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: PETERS, VERNY, JONES & BIKŠA  
(B) STREET: 385 Sherman Avenue, Suite 6  
(C) CITY: Palo Alto  
(D) STATE: California  
(E) COUNTRY: United States of America  
(F) ZIP: 94306-1840
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage  
(B) COMPUTER: PC  
(C) OPERATING SYSTEM: WINDOWS  
(D) SOFTWARE: Wordperfect 6.0a WINDOWS
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 60/014,233  
(B) FILING DATE: March 27, 1996
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Hana Verny  
(B) REGISTRATION NUMBER: 30,518  
(C) REFERENCE/DOCKET NUMBER: (HV)
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (415) 324-1677  
(B) TELEFAX: (415) 324-1678

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1663 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Cryptosporidium parvum*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CAAAACTTCC	TAATTTCTCA	ATGTATTACT	AATTAATAGA	AAGTTTGTTT	TATTTTCATG	60
TGGATAAATG	AATTATTTTC	TCTATACCGG	CATTTCATG	CAATTTTGTA	TGACTAAAAT	120
GTAAATAATT	ATTTGCATGC	AATTATGTGG	GCATGTCATA	GTTTTTCAAG	AATAATAATA	180
AGATGACATG	ACAAGATATT	CAAAAAAATT	TGATGATTAT	ATGTTGAAGT	TAATTGAACT	240
AAAAAGTAAT	TAAGTAAAT	GGACATAGGA	AACAACGTGG	AAGAACATCA	GGAATATATT	300
TCTGGACCAT	ACATTGCATT	AATTAATGGC	ACTAATCAAC	AAAGGGAACC	GAATAAAAAG	360

TTGAAAAACA	TAATAATTGC	AACGTTGATT	GCAATCTTTA	TAGTTTTGGT	TGTTACTGTA	420
TCTTTGTATA	TTACTAATAA	CACCAGTGAC	AAAATTGACG	ATTTTCGTACC	TGGTGATTAT	480
GTTGATCCAG	CAACTAGGGA	GTATAGAAAG	AGTTTTGAGG	AGTTCAAAAA	GAAATACCAC	540
AAAGTATATA	GCTCTATTGA	GGAGGAAAAA	CAAAGATTTC	AAATTTATAA	GCAAAATATG	600
AACTTTATTA	AAACAACAAA	TAGCCAAGGA	TTCAGTTATG	TGTTAGAAAT	GAATGAATTT	660
GGTGATTTGT	CGAAAGAAGA	GTTTATGGCA	AGATTCACAG	GATATATAAA	AGATTCCAAA	720
GATGATGAAA	GGGTATTTAA	GTCAAGTAGA	GTCTCAGCAA	GCGAATCAGA	AGAGGAATTT	780
GTTCCCCCAA	ATTCTATTAA	TTGGGTGGAA	GCTGGATGCG	TGAACCCAAT	AAGAAATCAA	840
AAGAATTGTG	GGTCATGTTG	GGCTTTCTCT	GCTGTTGCAG	CTTTGGAGGG	AGCAACGTGT	900
GCTCAAACAA	ACCGAGGATT	ACCAAGCTTG	AGTGAACAGC	AATTTGTTGA	TTGCAGTAAA	960
CAAAATGGCA	ACTTTGGATG	TGATGGAGGA	ACAATGGGAT	TGGCTTTTCA	GTATGCAATT	1020
AAGAACAAAT	ATTTATGTAC	TAATGATGAT	TACCCTTACT	TTGCTGAGGA	AAAAACATGT	1080
ATGGATTTCAT	TTTGCAGAGAA	TTATATAGAG	ATTCTGTAA	AAGCCTACAA	ATATGTATTT	1140
CCGAGAAATA	TTAATGCATT	AAAGACTGCT	TTGGCTAAGT	ATGGACCAAT	TTCAGTTGCA	1200
ATTCAGGCCG	ATCAAACCCC	TTTCCAGTTT	TATAAAAGTG	GAGTATTCGA	TGCTCCTTGT	1260
GGAACCAAGG	TTAATCATGG	AGTTGTTCTA	GTTGAATATG	ATATGGATGA	AGATACTAAT	1320
AAAGAATATT	GGCTAGTAAG	AAATAGCTGG	GGTGAAGCGT	GGGGAGAGAA	AGGATACATC	1380
AAACTAGCTC	TTCATTCTGG	AAAGAAGGGA	ACATGTGGTA	TATTGGTTGA	GCCAGTGTAT	1440
CCAGTGATTA	ATCAATCAAT	ATAAGCATTT	CAGTGTTTGA	CTAAGTAATT	CTAATATATT	1500
TCAGCATTCT	CAGAGATAAT	TTTAGTTCAA	ATGAACAATC	TATTCATATA	TATAAGCATT	1560
CCATACTTAA	TTATTTATTG	ATTTTAATAA	AATGTTTGGC	TAAAGAAAGC	AATCAAGATA	1620
ATTTATGGAC	GTTCTATTGT	TCTTACTTCA	ATAATAATCC	TTT		1663

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

TTAAGTAAAA	TGGACATAGG	AAACAACGTG	GAAGAACATC	AGGAATATAT	TTCTGGACCA	60
TACATTGCAT	TAATTAATGG	CACTAATCAA	CAAAGGGAAC	CGAATAAAAA	GTTGAAAAAC	120
ATAATAATTG	CAACGTTGAT	TGCAATCTTT	ATAGTTTTGG	TTGTTACTGT	ATCTTTGTAT	180
ATTACTAATA	ACACCAGTGA	CAAAATTGAC	GATTCGTAC	CTGGTGATTA	TGTTGATCCA	240
GCAACTAGGG	AGTATAGAAA	GAGTTTTGAG	GAGTTCAAAA	AGAAATACCA	CAAAGTATAT	300
AGCTCTATGG	AGGAGGAAAA	TCAAAGATTT	GAAATTTATA	AGCAAAATAT	GAACCTTATT	360
AAAACAACAA	ATAGCCAAGG	ATTCAGTTAT	GTGTTAGAAA	TGAATGAATT	TGGTGATTTG	420
TCGAAAGAAG	AGTTTATGGC	AAGATTCACA	GGATATATAA	AAGATTCCAA	AGATGATGAA	480
AGGGTATTTA	AGTCAAGTAG	AGTCTCAGCA	AGCGAATCAG	AAGAGGAATT	TGTT	534

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CCCCCAAATT	CTATTAATTG	GGTGAAGCT	GGATGCGTGA	ACCCAATAAG	AAATCAAAAG	60
AATTGTGGGT	CATGTTGGGC	TTTCTCTGCT	GTTGCAGCTT	TGGAGGGAGC	AACGTGTGCT	120
CAAACAAACC	GAGGATTACC	AAGCTTGAGT	GAACAGCAAT	TTGTTGATTG	CAGTAAACAA	180
AATGGCAACT	TTGGATGTGA	TGGAGGAACA	ATGGGATTGG	CTTTTCAGTA	TGCAATTAAG	240
AACAAATATT	TATGTACTAA	TGATGATTAC	CCTTACTTTG	CTGAGGAAAA	AACATGTATG	300
GATTCATTTT	GCGAGAATTA	TATAGAGATT	CCTGTAAAAAG	CCTACAAATA	TGTATTTCCG	360
AGAAATATTA	ATGCATTAAA	GACTGCTTTG	GCTAAGTATG	GACCAATTTT	AGTTGCAATT	420
CAGGCCGATC	AAACCCCTTT	CCAGTTTAT	AAAAGTGGAG	TATTCGATGC	TCCTTGTTGA	480
ACCAAGGTTA	ATCATGGAGT	TGTTCTAGTT	GAATATGATA	TGGATGAAGA	TACTAATAAA	540
GAATATTGGC	TAGTAAGAAA	TAGCTGGGGT	GAAGCGTGGG	GAGAGAAAAG	ATACATCAAA	600
CTAGCTCTTC	ATTCTGGAAA	GAAGGGAACA	TGTGGTATAT	TGGTTGAGCC	AGTGTATCCA	660
GTGATTAATC	AATCAATA					678

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 amino acids

(B) TYPE: amino acids

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Asp	Ile	Gly	Asn	Asn	Val	Glu	Glu	His	Gln	Glu	Tyr	Ile	Ser
1				5					10					15
Gly	Pro	Tyr	Ile	Ala	Leu	Ile	Asn	Gly	Thr	Asn	Gln	Gln	Arg	Glu
				20					25					30
Pro	Asn	Lys	Lys	Leu	Lys	Asn	Ile	Ile	Ile	Ala	Thr	Leu	Ile	Ala
				35					40					45
Ile	Phe	Ile	Val	Leu	Val	Val	Thr	Val	Ser	Leu	Tyr	Ile	Thr	Asn
				50					55					60
Asn	Thr	Ser	Asp	Lys	Ile	Asp	Asp	Phe	Val	Pro	Gly	Asp	Tyr	Val
				65					70					75
Asp	Pro	Ala	Thr	Arg	Glu	Tyr	Arg	Lys	Ser	Phe	Glu	Glu	Phe	Lys
				80					85					90
Lys	Lys	Tyr	His	Lys	Val	Tyr	Ser	Ser	Met	Glu	Glu	Glu	Asn	Gln
				95					100					105
Arg	Phe	Glu	Ile	Tyr	Lys	Gln	Asn	Met	Asn	Phe	Ile	Lys	Thr	Thr
				110					115					120
Asn	Ser	Gln	Gly	Phe	Ser	Tyr	Val	Leu	Glu	Met	Asn	Glu	Phe	Gly
				125					130					135
Asp	Leu	Ser	Lys	Glu	Glu	Phe	Met	Ala	Arg	Phe	Thr	Gly	Tyr	Ile
				140					145					150
Lys	Asp	Ser	Lys	Asp	Asp	Glu	Arg	Val	Phe	Lys	Ser	Ser	Arg	Val
				155					160					165
Ser	Ala	Ser	Glu	Ser	Glu	Glu	Glu	Phe	Val	Pro	Pro	Asn	Ser	Ile
				170					175					180
Asn	Trp	Val	Glu	Ala	Gly	Cys	Val	Asn	Pro	Ile	Arg	Asn	Gln	Lys
				185					190					195
Asn	Cys	Gly	Ser	Cys	Trp	Ala	Phe	Ser	Ala	Val	Ala	Ala	Leu	Glu
				200					205					210

Gly	Ala	Thr	Cys	Ala	Gln	Thr	Asn	Arg	Gly	Leu	Pro	Ser	Leu	Ser	215	220	225
Glu	Gln	Gln	Phe	Val	Asp	Cys	Ser	Lys	Gln	Asn	Gly	Asn	Phe	Gly	230	235	240
Cys	Asp	Gly	Gly	Thr	Met	Gly	Leu	Ala	Phe	Gln	Tyr	Ala	Ile	Lys	245	250	255
Asn	Lys	Tyr	Leu	Cys	Thr	Asn	Asp	Asp	Tyr	Pro	Tyr	Phe	Ala	Glu	260	265	270
Glu	Lys	Thr	Cys	Met	Asp	Ser	Phe	Cys	Glu	Asn	Tyr	Ile	Glu	Ile	275	280	285
Pro	Val	Lys	Ala	Tyr	Lys	Tyr	Val	Phe	Pro	Arg	Asn	Ile	Asn	Ala	290	295	300
Leu	Lys	Thr	Ala	Leu	Ala	Lys	Tyr	Gly	Pro	Ile	Ser	Val	Ala	Ile	305	310	315
Gln	Ala	Asp	Gln	Thr	Pro	Phe	Gln	Phe	Tyr	Lys	Ser	Gly	Val	Phe	320	325	330
Asp	Ala	Pro	Cys	Gly	Thr	Lys	Val	Asn	His	Gly	Val	Val	Leu	Val	335	340	345
Glu	Tyr	Asp	Met	Asp	Glu	Asp	Thr	Asn	Lys	Glu	Tyr	Trp	Leu	Val	350	355	360
Arg	Asn	Ser	trp	Gly	Glu	Ala	Trp	Gly	Glu	Lys	Gly	Tyr	Ile	Lys	365	370	375
Leu	Ala	Leu	His	Ser	Gly	Lys	Lys	Gly	Thr	Cys	Gly	Ile	Leu	Val	380	385	390
Glu	Pro	Val	Tyr	Pro	Val	Ile	Asn	Gln	Ser	Ile					395	400	403

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Met	Asp	Ile	Gly	Asn	Asn	Val	Glu	Glu	His	Gln	Glu	Tyr	Ile	Ser	1	5	10	15
Gly	Pro	Tyr	Ile	Ala	Leu	Ile	Asn	Gly	Thr	Asn	Gln	Gln	Arg	Glu	20	25	30	35
Pro	Asn	Lys	Lys	Leu	Lys	Asn	Ile	Ile	Ile	Ala	Thr	Leu	Ile	Ala	40	45	50	55
Ile	Phe	Ile	Val	Leu	Val	Val	Thr	Val	Ser	Leu	Tyr	Ile	Thr	Asn	60	65	70	75
Asn	Thr	Ser	Asp	Lys	Ile	Asp	Asp	Phe	Val	Pro	Gly	Asp	Tyr	Val	80	85	90	95
Asp	Pro	Ala	Thr	Arg	Glu	Tyr	Arg	Lys	Ser	Phe	Glu	Glu	Phe	Lys	100	105	110	115
Lys	Lys	Tyr	His	Lys	Val	Tyr	Ser	Ser	Met	Glu	Glu	Glu	Asn	Gln	120	125	130	135
Arg	Phe	Glu	Ile	Tyr	Lys	Gln	Asn	Met	Asn	Phe	Ile	Lys	Thr	Thr	140	145	150	155
Asn	Ser	Gln	Gly	Phe	Ser	Tyr	Val	Leu	Glu	Met	Asn	Glu	Phe	Gly	160	165	170	175

	125		130		135
Asp Leu Ser Lys	Glu Glu Phe Met Ala Arg	Phe Thr Gly Tyr Ile			
	140		145		150
Lys Asp Ser Lys	Asp Asp Glu Arg Val Phe	Lys Ser Ser Arg Val			
	155		160		165
Ser Ala Ser Glu	Ser Glu Glu Glu Phe Val				
	170		175		

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Pro	Pro	Asn	Ser	Ile	Asn	Trp	Val	Glu	Ala	Gly	Cys	Val	Asn	Pro
1				5					10					15
Ile	Arg	Asn	Gln	Lys	Asn	Cys	Gly	Ser	Cys	Trp	Ala	Phe	Ser	Ala
				20					25					30
Val	Ala	Ala	Leu	Glu	Gly	Ala	Thr	Cys	Ala	Gln	Thr	Asn	Arg	Gly
				35					40					45
Leu	Pro	Ser	Leu	Ser	Glu	Gln	gln	Phe	Val	Asp	Cys	Ser	Lys	Gln
				50					55					60
Asn	Gly	Asn	Phe	Gly	Cys	Asp	Gly	Gly	Thr	Met	Gly	Leu	Ala	Phe
				65					70					75
Gln	Tyr	Ala	Ile	Lys	Asn	Lys	Tyr	Leu	Cys	Thr	Asn	Asp	Asp	Tyr
				80					85					90
Pro	Tyr	Phe	Ala	Glu	Glu	Lys	Thr	Cys	Met	Asp	Ser	Phe	Cys	Glu
				95					100					105
Asn	Tyr	Ile	Glu	Ile	Pro	Val	Lys	Ala	Tyr	Lys	Tyr	Val	Phe	Pro
				110					115					120
Arg	Asn	Ile	Asn	Ala	Leu	Lys	Thr	Ala	Leu	Ala	Lys	Tyr	Gly	Pro
				125					130					135
Ile	Ser	Val	Ala	Ile	Gln	Ala	Asp	Gln	Thr	Pro	Phe	Gln	Phe	Tyr
				140					145					150
Lys	Ser	Gly	Val	Phe	Asp	Ala	Pro	Cys	Gly	Thr	Lys	Val	Asn	His
				155					160					165
Gly	Val	Val	Leu	Val	Glu	Tyr	Asp	Met	Asp	Glu	Asp	Thr	Asn	Lys
				170					175					180
Glu	Tyr	Trp	Leu	Val	Arg	Asn	Ser	Trp	Gly	Glu	Ala	Trp	Gly	Glu
				185					190					195
Lys	Gly	Tyr	Ile	Lys	Leu	Ala	Leu	His	Ser	Gly	Lys	Lys	Gly	Thr
				200					205					210
Cys	Gly	Ile	Leu	Val	Glu	Pro	Val	Tyr	Pro	Val	Ile	asn	Gln	Ser
				215					220					225
Ile														
226														

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Carica

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met	Ala	Met	Ile	Pro	Ser	Ile	Ser	Lys	Leu	Leu	Phe	Val	Ala	Ile	5	10	15
Cys	Leu	Phe	Val	Tyr	Met	Gly	Leu	Ser	Phe	Gly	Asp	Phe	Ser	Ile	20	25	30
Val	Gly	Tyr	Ser	Gln	Asn	Asp	Leu	Thr	Ser	Thr	Glu	Arg	Leu	Ile	35	40	45
Gln	Leu	Phe	Glu	Ser	Trp	Met	Leu	Lys	His	Asn	Lys	Ile	Tyr	Lys	50	55	60
Asn	Ile	Asp	Glu	Lys	Ile	Tyr	Arg	Phe	Glu	Ile	Phe	Lys	Asp	Asn	65	70	75
Leu	Lys	Tyr	Ile	Asp	Glu	Thr	Asn	Lys	Lys	Asn	Asn	Ser	Tyr	Trp	80	85	90
Leu	Gly	Leu	Asn	Val	Phe	Ala	Asp	Met	Ser	Asn	Asp	Glu	Phe	Lys	95	100	105
Glu	Lys	Tyr	Thr	Gly	Ser	Ile	Ala	Gly	Asn	Tyr	Thr	Thr	Thr	Glu	110	115	120
Leu	Ser	Tyr	Glu	Glu	Val	Leu	Asn	Asp	Gly	Asp	Val	Asn	Ile	Pro	125	130	135
Glu	Tyr	Val	Asp	Trp	Arg	Gln	Lys	Gly	Ala	Val	Thr	Pro	Val	Lys	140	145	150
Asn	Gln	Gly	Ser	Cys	Gly	Ser	Cys	Trp	Ala	Phe	Ser	Ala	Val	Val	155	160	165
Thr	Ile	Glu	Gly	Ile	Ile	Lys	Ile	Arg	Thr	Gly	Asn	Leu	Asn	Glu	170	175	180
Tyr	Ser	Glu	Gln	Glu	Leu	Leu	Asp	Cys	Asp	Arg	Arg	Ser	Tyr	Gly	185	190	195
Cys	Asn	Gly	Gly	Tyr	Pro	Trp	Ser	Ala	Leu	Gln	Leu	Val	Ala	Gln	200	205	210
Tyr	Gly	Ile	His	Tyr	Arg	Asn	Thr	Tyr	Pro	Tyr	Glu	Gly	Val	Gln	215	220	225
Arg	Tyr	Cys	Arg	Ser	Arg	Glu	Lys	Gly	Pro	Tyr	Ala	Ala	Lys	Thr	230	235	240
Asp	Gly	Val	Arg	Gln	Val	Gln	Pro	Tyr	Asn	Glu	Gly	Ala	Leu	Leu	245	250	255
Tyr	Ser	Ile	Ala	Asn	Gln	Pro	Val	Ser	Val	Val	Leu	Glu	Ala	Ala	260	265	270
Gly	Lys	Asp	Phe	Gln	Leu	Tyr	Arg	Gly	Gly	Ile	Phe	Val	Gly	Pro	275	280	285
Cys	Gly	Asn	Lys	Val	Asp	His	Ala	Val	Ala	Ala	Val	Gly	Tyr	Gly	290	295	300
Pro	Asn	Tyr	Ile	Leu	Ile	Lys	Asn	Ser	Trp	Gly	Thr	Gly	Trp	Gly	305	310	315
Glu	Asn	Gly	Tyr	Ile	Arg	Ile	Lys	Arg	Gly	Thr	Gly	Asn	Ser	Tyr	320	325	330
Gly	Val	Cys	Gly	Leu	Tyr	Thr	Ser	Ser	Phe	Tyr	Pro	Val	Lys	Asn	335	340	345

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Plasmodium vinckei

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Phe	Pro	Asp	Ser	Arg	Asp	Tyr	Arg	Ser	Lys	Phe	Asn	Phe	Leu	Pro
				5					10					15
Pro	Lys	Asp	Gln	Gly	Asn	Cys	Gly	Ser	Cys	trp	Ala	Phe	Ala	Ala
				20					25					30
Ile	Gly	Asn	Phe	Glu	Tyr	Leu	Tyr	Val	His	Thr	Arg	His	Glu	Met
				35					40					45
Pro	Ile	Ser	Phe	Ser	Glu	Gln	Gln	Met	Val	Asp	Cys	Ser	Thr	Glu
				50					55					60
Asn	Tyr	Gly	Cys	Asp	Gly	Gly	Asn	Pro	Phe	Tyr	Ala	Phe	Leu	Tyr
				65					70					75
Met	Ile	Asn	Asn	Gly	Val	Cys	Leu	Gly	Asp	Glu	Tyr	Pro	Tyr	Lys
				80					85					90
Gly	His	Glu	Asp	Phe	Phe	Cys	Leu	Asn	Tyr	Arg	Cys	Ser	Leu	Leu
				95					100					105
Gly	Arg	Val	His	Phe	Ile	Gly	Asp	Val	Lys	Pro	Asn	Glu	Leu	Ile
				110					115					120
Met	Ala	Leu	Asn	Tyr	Val	Gly	Pro	Val	Thr	Ile	Ala	Val	Gly	Ala
				125					130					135
Ser	Glu	Asp	Phe	Val	Leu	Tyr	Ser	Gly	Gly	Val	Phe	Asp	Gly	Glu
				140					145					150
Cys	Asn	Pro	Glu	Leu	Asn	His	Ser	Val	Leu	Leu	Val	Gly	Tyr	Gly
				155					160					165
Gln	Val	Lys	Lys	Ser	Leu	Ala	Phe	Glu	Asp	Ser	His	Ser	Asn	Val
				170					175					180
Asp	Ser	Asn	Leu	Ile	Lys	Lys	Tyr	Lys	Glu	Asn	Ile	Lys	Gly	Asp
				185					190					195
Asp	Asp	Asp	Asp	Ile	Ile	Tyr	Tyr	Trp	Ile	Val	Arg	Asn	Ser	Trp
				200					205					210
Gly	Pro	Asn	Trp	Gly	Glu	Gly	Gly	Tyr	Ile	Arg	Ile	Lys	Arg	Asn
				215					220					225
Lys	Ala	Gly	Asp	Asp	Gly	Phe	Cys	Gly	Val	Gly	Ser	Asp	Val	Phe
				230					235					240
Phe	Pro	Ile	Tyr											
				244										

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic oligonucleotide

(ix) FEATURE:

(A) NAME/KEY:

Y is C/T

W is A/T

S is C/G

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

AAAGGATCCT GYGGNWSNTG YTGGGCNTT

29

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic oligonucleotide

(ix) FEATURE:

(A) NAME/KEY:

S is C/G

K is G/T

W is A/T

R is A/G

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

TTTGAATTCC CANSWRRTNY KNAYNATCCA RTA

33

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CCAGGTACCA TGGACATAGG AAAC

24

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic oligonucleotide



- (iv) ANTI- SENSE: YES
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CCCTCTAGAT GCTTATATTG ATTG

24

- (2) INFORMATION FOR SEQ ID NO: 13:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 7 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Cys Gly Ser Cys Trp Ala Phe  
5 7

- (2) INFORMATION FOR SEQ ID NO: 14:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 8 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptides
  - (ix) FEATURE:
    - (A) NAME/KEY:
      - Xaa at 4 is Val/Ile
      - Xaa at 5 is Lys/Arg
    - (B) LOCATION:
    - (C) IDENTIFICATION METHOD:
    - (D) OTHER INFORMATION:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Tyr Trp Ile Xaa Xaa Asn Ser Trp  
5 8

- (2) INFORMATION FOR SEQ ID NO: 15:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 5 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Val Arg Asn Ser Trp  
5

- (2) INFORMATION FOR SEQ ID NO: 16:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1203 base pairs

- (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: DNA  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Cryptosporidium parvum*  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ATGGACATAG	GAAACAACGT	GGAAGAACAT	CAGGAATATA	TTTCTGGACC	ATACATTGCA	60
TTAATTAATG	GCACTAATCA	ACAAAGGGAA	CCGAATAAAA	AGTTGAAAAA	CATAATAATT	120
GCAACGTTGA	TTGCAATCTT	TATAGTTTTG	GTTGTTACTG	TATCTTTGTA	TATTACTAAT	180
AACACCAGTG	ACAAAATTGA	CGATTTTCGT	CCTGGTGATT	ATGTTGATCC	AGCAACTAGG	240
GAGTATAGAA	AGAGTTTGA	GGAGTTCAAA	AAGAAATACC	ACAAAGTATA	TAGCTCTATG	300
GAGGAGGAAA	ATCAAAGATT	TGAAATTTAT	AAGCAAAATA	TGAACTTTAT	TAAAACAACA	360
AATAGCCAAG	GATTCAGTTA	TGTGTTAGAA	ATGAATGAAT	TTGGTGATTT	GTCGAAAGAA	420
GAGTTTATGG	CAAGATTCAC	AGGATATATA	AAAGATTCCA	AAGATGATGA	AAGGGTATTT	480
AAGTCAAGTA	GAGTCTCAGC	AAGCGAATCA	GAAGAGGAAT	TTGTTCCCCC	AAATTCTATT	540
AATTGGGTGG	AAGCTGGATG	CGTGAACCCA	ATAAGAAATC	AAAAGAATTG	TGGGTCATGT	600
TGGGCTTTCT	CTGCTGTTGC	AGCTTTGGAG	GGAGCAACGT	GTGCTCAAAC	AAACCGAGGA	660
TTACCAAGCT	TGAGTGAACA	GCAATTTGTT	GATTGCAGTA	AACAAAATGG	CAACTTTGGA	720
TGTGATGGAG	GAACAATGGG	ATTGGCTTTT	CAGTATGCAA	TTAAGAACAA	ATATTTATGT	780
ACTAATGATG	ATTACCCTTA	CTTTGCTGAG	GAAAAAACAT	GTATGGATTC	ATTTTGCGAG	840
AATTATATAG	AGATTCCTGT	AAAAGCCTAC	AAATATGTAT	TTCCGAGAAA	TATTAATGCA	900
TTAAAGACTG	CTTTGGCTAA	GTATGGACCA	ATTTCAAGTG	CAATTCAGGC	CGATCAAACC	960
CCTTTCCAGT	TTTATAAAAAG	TGGAGTATTC	GATGCTCCTT	GTGGAACCAA	GGTTAATCAT	1020
GGAGTTGTTT	TAGTTGAATA	TGATATGGAT	GAAGATACTA	ATAAAGAATA	TTGGCTAGTA	1080
AGAAATAGCT	GGGGTGAAGC	GTGGGGAGAG	AAAGGATACA	TCAAAC TAGC	TCTTCATTCT	1140
GGAAAGAAGG	GAACATGTGG	TATATTGGTT	GAGCCAGTGT	ATCCAGTGAT	TAATCAATCA	1200
ATA						1203

SEQUENCE LISTING

5

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

CAROLYN PETERSEN  
JIN-XING HUANG

10

## (ii) TITLE OF INVENTION:

CRYPTOPAIN VACCINES,  
ANTIBODIES, PROTEINS, PEPTIDES,  
DNA AND RNAs FOR PROPHYLAXIS,  
TREATMENT, DIAGNOSIS AND  
DETECTION OF  
CRYPTOSPORIDIUM PARVUM

15

## (iii) NUMBER OF SEQUENCES: 15

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: PETERS, VERNY, JONES & BIKŠA  
(B) STREET: 385 Sherman Avenue, Suite 6  
(C) CITY: Palo Alto  
(D) STATE: California  
(E) COUNTRY: United States of America  
(F) ZIP: 94306-1840

20

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage  
(B) COMPUTER: PC  
(C) OPERATING SYSTEM: WINDOWS  
(D) SOFTWARE: Wordperfect 6.0a WINDOWS

25

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

30

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/014,233  
(B) FILING DATE: March 27, 1996

35

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Hana Verny  
(B) REGISTRATION NUMBER: 30,518  
(C) REFERENCE/DOCKET NUMBER: (HV)

40

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (415) 324-1677  
(B) TELEFAX: (415) 324-1678

45

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1663 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

## (ii) MOLECULE TYPE: DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

55

60

CAAAACTTCC	TAATTTCTCA	ATGTATTACT	AATTAATAGA	AAGTTTGTTT	TATTTTCATG	60
TGGATAAATG	AATTATTTTC	TCTATACCGG	CATTGTCATG	CAATTTTGTA	TGACTAAAAT	120
GTAAATAAAT	ATTGTCATGC	AATTATGTGG	GCATGTCATA	GTTTTTCAAG	AATAATAATA	180
AGATGACATG	ACAAGATATT	CAAAAAAATT	TGATGATTAT	ATGTTGAAGT	TAATTGAACT	240
AAAAAGTAAT	TAAGTAAAT	GGACATAGGA	AACAACGTGG	AAGAACATCA	GGAATATATT	300
TCTGGACCAT	ACATTGCATT	AATTAATGGC	ACTAATCAAC	AAAGGGAACC	GAATAAAAAG	360
TTGAAAAACA	TAATAATTGC	AACGTTGATT	GCAATCTTTA	TAGTTTGGT	TGTTACTGTA	420

	TCTTTGTATA	TTACTAATAA	CACCAGTGAC	AAAATTGACG	ATTTCGTACC	TGGTGATTAT	480
	GTTGATCCAG	CAACTAGGGA	GTATAGAAAG	AGTTTGGAGG	AGTTCAAAAA	GAAATACCAC	540
	AAAGTATATA	GCTCTATGGA	GGAGGAAAAT	CAAAGATTG	AAATTTATAA	GCAAAATATG	600
	AACTTTATTA	AAACAACAAA	TAGCCAAGGA	TTCAGTTATG	TGTTAGAAAT	GAATGAATTT	660
5	GGTGATTTGT	CGAAAGAAGA	GTTTATGGCA	AGATTCACAG	GATATATAAA	AGATTCCAAA	720
	GATGATGAAA	GGGTATTTAA	GTCAAGTAGA	GTCTCAGCAA	GCGAATCAGA	AGAGGAATTT	780
	GTTCCCCCAA	ATTCTATTAA	TTGGGTGGAA	GCTGGATGCG	TGAACCCAA	AAGAAATCAA	840
	AAGAATTGTG	GGTCATGTTG	GGCTTCTCT	GCTGTTGCAG	CTTTGGAGGG	AGCAACGTGT	900
	GCTCAAACAA	ACCGAGGATT	ACCAAGCTTG	AGTGAACAGC	AATTTGTTGA	TTGCAGTAAA	960
10	CAAAATGGCA	ACTTTGGATG	TGATGGAGGA	ACAAATGGGAT	TGGCTTTTCA	GTATGCAATT	1020
	AAGAACAAAT	ATTTATGTAC	TAATGATGAT	TACCCTTACT	TTGCTGAGGA	AAAAACATGT	1080
	ATGGATTCAT	TTTGCGAGAA	TTATATAGAG	ATTCCCTGTA	AAGCCTACAA	ATATGTATTT	1140
	CCGAGAAATA	TTAATGCATT	AAAGACTGCT	TTGGCTAAGT	ATGGACCAAT	TTCAAGTTGCA	1200
	ATTCAGGCCG	ATCAAACCCC	TTTCCAGTTT	TATAAAAGTG	GAGTATTCGA	TGCTCCTTGT	1260
15	GGAACCAAGG	TTAATCATGG	AGTTGTTCTA	GTTGAATATG	ATATGGATGA	AGATACTAAT	1320
	AAAGAATATT	GGCTAGTAAG	AAATAGCTGG	GGTGAAGCGT	GGGGAGAGAA	AGGATACATC	1380
	AAACTAGCTC	TTCATTCTGG	AAAGAAGGGA	ACATGTGGTA	TATTGGTTGA	GCCAGTGTAT	1440
	CCAGTGATTA	ATCAATCAAT	ATAAGCATTT	CAGTGTGTTA	CTAAGTAATT	CTAATATATT	1500
	TCAGCATTTCT	CAGAGATAAT	TTTAGTTCAA	ATGAACAATC	TATTCATATA	TATAAGCATT	1560
20	CCATACTTAA	TTATTTATTG	ATTTTAATAA	ATGTTTGGC	TAAAGAAAGC	AATCAAGATA	1620
	ATTTATGGAC	GTTCTATTGT	TCTTACTTCA	ATAATAATCC	TTT		1663

## (2) INFORMATION FOR SEQ ID NO: 2:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

## (ii) MOLECULE TYPE: DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

35	TTAAGTAAAA	TGGACATAGG	AAACAACGTG	GAAGAACATC	AGGAATATAT	TTCTGGACCA	60
	TACATTGCAT	TAATTAATGG	CACTAATCAA	CAAAGGGAAC	CGAATAAAAA	GTTGAAAAAC	120
	ATAATAATTG	CAACGTTGAT	TGCAATCTTT	ATAGTTTTGG	TTGTTACTGT	ATCTTTGTAT	180
	ATTACTAATA	ACACCAGTGA	CAAAATTGAC	GATTTTCGTAC	CTGGTGATTA	TGTTGATCCA	240
	GCAACTAGGG	AGTATAGAAA	GAGTTTTGAG	GAGTTCAAAA	AGAAATACCA	CAAAGTATAT	300
40	AGCTCTATGG	AGGAGGAAAA	TCAAAGATTT	GAAATTTATA	AGCAAAATAT	GAACTTTATT	360
	AAAACAACAA	ATAGCCAAGG	ATTCAAGTTAT	GTGTTAGAAA	TGAATGAATT	TGGTGATTTG	420
	TCGAAAGAAG	AGTTTATGGC	AAGATTCCAA	GGATATATAA	AAGATTCCAA	AGATGATGAA	480
	AGGGTATTTA	AGTCAAGTAG	AGTCTCAGCA	AGCGAATCAG	AAGAGGAATT	TGTT	534

45

## (2) INFORMATION FOR SEQ ID NO: 3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

50

## (ii) MOLECULE TYPE: DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

	CCCCCAAATT	CTATTAATTG	GGTGAAGCT	GGATGCGTGA	ACCCAATAAG	AAATCAAAAG	60
	AATTGTGGGT	CATGTTGGGC	TTTCTCTGCT	GTTGCAGCTT	TGGAGGGAGC	AACGTGTGCT	120
60	CAAAACAAACC	GAGGATTACC	AAGCTTGAGT	GAACAGCAAT	TTGTTGATTG	CAGTAAACAA	180
	AATGGCAACT	TTGGATGTGA	TGGAGGAACA	ATGGGATTGG	CTTTTCAGTA	TGCAATTAAG	240
	AACAAATATT	TATGTACTAA	TGATGATTAC	CCTTACTTTG	CTGAGGAAAA	AACATGTATG	300

GATTCATTTT GCGAGAATTA TATAGAGATT CCTGTAAAAG CCTACAAATA TGTATTTCCG 360  
 AGAAATATTA ATGCATTAAA GACTGCTTTG GCTAAGTATG GACCAATTTC AGTTGCAATT 420  
 CAGGCCGATC AAACCCCTTT CCAGTTTTAT AAAAGTGGAG TATTCGATGC TCCTTGTGGA 480  
 ACCAAGGTTA ATCATGGAGT TGTCTAGTT GAATATGATA TGGATGAAGA TACTAATAAA 540  
 5 GAATATTGGC TAGTAAGAAA TAGCTGGGGT GAAGCGTGGG GAGAGAAAGG ATACATCAAA 600  
 CTAGCTCTTC ATTCTGGAAA GAAGGGAACA TGTGGTATAT TGGTTGAGCC AGTGTATCCA 660  
 GTGATTAATC AATCAATA 678

## (2) INFORMATION FOR SEQ ID NO: 4:

- 10 (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 401 amino acids  
     (B) TYPE: amino acids  
     (C) STRANDEDNESS: single  
     (D) TOPOLOGY: linear  
 15 (ii) MOLECULE TYPE: protein  
     (vi) ORIGINAL SOURCE:  
         (A) ORGANISM: *Cryptosporidium parvum*  
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

20 met asp ile gly asn asn val glu glu his gln glu tyr ile ser  
     1                    5                    10  
 gly pro tyr ile ala leu ile asn gly thr asn gln gln arg glu  
                     20                    25                    30  
 25 pro asn lys lys leu lys asn ile ile ala thr leu ile ala  
                     35                    40                    45  
 ile phe ile val leu val val thr val ser leu tyr ile thr asn  
                     50                    55                    60  
 asn thr ser asp lys ile asp asp phe val pro gly asp tyr val  
                     65                    70                    75  
 30 asp pro ala thr arg glu tyr arg lys ser phe glu glu phe lys  
                     80                    85                    90  
 lys lys tyr his lys val tyr ser ser met glu glu glu asn gln  
                     95                    100                    105  
 arg phe glu ile tyr lys gln asn met asn phe ile lys thr thr  
                     110                    115                    120  
 35 asn ser gln gly phe ser tyr val leu glu met asn glu phe gly  
                     125                    130                    135  
 asp leu ser lys glu glu phe met ala arg phe thr gly tyr ile  
                     140                    145                    150  
 40 lys asp ser lys asp asp glu arg val phe lys ser ser arg val  
                     155                    160                    165  
 ser ala ser glu ser glu glu glu phe val pro pro asn ser ile  
                     170                    175                    180  
 45 asn trp val glu ala gly cys val asn pro ile arg asn gln lys  
                     185                    190                    195  
 asn cys gly ser cys trp ala phe ser ala val ala ala leu glu  
                     200                    205                    210  
 gly ala thr cys ala gln thr asn arg gly leu pro ser leu ser  
                     215                    220                    225  
 50 glu gln gln phe val asp cys ser lys gln asn gly asn phe gly  
                     230                    235                    240  
 cys asp gly gly thr met gly leu ala phe gln tyr ala ile lys  
                     245                    250                    255  
 55 asn lys tyr leu cys thr asn asp asp tyr pro tyr phe ala glu  
                     260                    265                    270  
 glu lys thr cys met asp ser phe cys glu asn tyr ile glu ile  
                     275                    280                    285  
 pro val lys ala tyr lys tyr val phe pro arg asn ile asn ala  
                     290                    295                    300  
 60 leu lys thr ala leu ala lys tyr gly pro ile ser val ala ile  
                     305                    310                    315  
 gln ala asp gln thr pro phe gln phe tyr lys ser gly val phe

		320		325		330
	asp	ala	pro	cys	gly	thr
		335		340	his	gly
	glu	tyr	asp	met	asp	glu
5		350		355	lys	glu
	arg	asn	ser	trp	gly	glu
		365		370	lys	gly
	leu	ala	leu	his	ser	gly
		380		385	thr	cys
10	glu	pro	val	tyr	pro	val
		395		400	403	

## (2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
- 15 (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- 20 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Cryptosporidium parvum*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

25	met	asp	ile	gly	asn	asn	val	glu	glu	his	gln	glu	tyr	ile	ser
	1			5				10							15
	gly	pro	tyr	ile	ala	leu	ile	asn	gly	thr	asn	gln	gln	arg	glu
				20				25							30
	pro	asn	lys	lys	leu	lys	asn	ile	ile	ile	ala	thr	leu	ile	ala
				35				40							45
30	ile	phe	ile	val	leu	val	val	thr	val	ser	leu	tyr	ile	thr	asn
				50				55							60
	asn	thr	ser	asp	lys	ile	asp	asp	phe	val	pro	gly	asp	tyr	val
				65				70							75
	asp	pro	ala	thr	arg	glu	tyr	arg	lys	ser	phe	glu	glu	phe	lys
35				80				85							90
	lys	lys	tyr	his	lys	val	tyr	ser	ser	met	glu	glu	glu	asn	gln
				95				100							105
	arg	phe	glu	ile	tyr	lys	gln	asn	met	asn	phe	ile	lys	thr	thr
				110				115							120
40	asn	ser	gln	gly	phe	ser	tyr	val	leu	glu	met	asn	glu	phe	gly
				125				130							135
	asp	leu	ser	lys	glu	glu	phe	met	ala	arg	phe	thr	gly	tyr	ile
				140				145							150
	lys	asp	ser	lys	asp	asp	glu	arg	val	phe	lys	ser	ser	arg	val
45				155				160							165
	ser	ala	ser	glu	ser	glu	glu	glu	phe	val					
				170				175							

## (2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
- 50 (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: protein
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Cryptosporidium parvum*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

60	pro	pro	asn	ser	ile	asn	trp	val	glu	ala	gly	cys	val	asn	pro
	1				5				10						15
	ile	arg	asn	gln	lys	asn	cys	gly	ser	cys	trp	ala	phe	ser	ala

		20		25		30
	val	ala	ala	leu	glu	gly
					ala	thr
					cys	ala
					gln	thr
					asn	arg
					gly	
					35	45
	leu	pro	ser	leu	ser	glu
					gln	gln
					phe	val
					asp	cys
					ser	lys
					gln	
5	asn	gly	asn	phe	gly	cys
					asp	gly
					gly	thr
					met	gly
					leu	ala
					phe	
					65	75
	gln	tyr	ala	ile	lys	asn
					lys	tyr
					leu	cys
					thr	asn
					asp	asp
					tyr	
					80	90
10	pro	tyr	phe	ala	glu	glu
					lys	thr
					cys	met
					asp	ser
					phe	cys
					glu	
					95	105
	asn	tyr	ile	glu	ile	pro
					val	lys
					ala	tyr
					lys	tyr
					val	phe
					pro	
					110	120
	arg	asn	ile	asn	ala	leu
					lys	thr
					ala	leu
					ala	lys
					tyr	gly
					pro	
15	ile	ser	val	ala	ile	gln
					ala	asp
					gln	thr
					pro	phe
					gln	phe
					tyr	
					125	135
	lys	ser	gly	val	phe	asp
					ala	pro
					cys	gly
					thr	lys
					val	asn
					his	
					155	165
20	gly	val	val	leu	val	glu
					tyr	asp
					met	asp
					glu	asp
					thr	asn
					lys	
					170	180
	glu	tyr	trp	leu	val	arg
					asn	ser
					trp	gly
					glu	ala
					trp	gly
					glu	
					185	195
	lys	gly	tyr	ile	lys	leu
					ala	leu
					his	ser
					gly	lys
					lys	gly
					thr	
25	cys	gly	ile	leu	val	glu
					pro	val
					ile	asn
					gln	ser
					215	225
	ile					
	226					

30

## (2) INFORMATION FOR SEQ ID NO: 7:

## (i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 345 amino acids

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vi) SOURCE ORIGIN:

40

(A) ORGANISM: Carica

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

	met	ala	met	ile	pro	ser	ile	ser	lys	leu	leu	phe	val	ala	ile
					5				10						15
	cys	leu	phe	val	tyr	met	gly	leu	ser	phe	gly	asp	phe	ser	ile
45					20				25						30
	val	gly	tyr	ser	gln	asn	asp	leu	thr	ser	thr	glu	arg	leu	ile
					35				40						45
	gln	leu	phe	glu	ser	trp	met	leu	lys	his	asn	lys	ile	tyr	lys
					50				55						60
50	asn	ile	asp	glu	lys	ile	tyr	arg	phe	glu	ile	phe	lys	asp	asn
					65				70						75
	leu	lys	tyr	ile	asp	glu	thr	asn	lys	lys	asn	asn	ser	tyr	trp
					80				85						90
	leu	gly	leu	asn	val	phe	ala	asp	met	ser	asn	asp	glu	phe	lys
55					95				100						105
	glu	lys	tyr	thr	gly	ser	ile	ala	gly	asn	tyr	thr	thr	thr	glu
					110				115						120
	leu	ser	tyr	glu	glu	val	leu	asn	asp	gly	asp	val	asn	ile	pro
					125				130						135
60	glu	tyr	val	asp	trp	arg	gln	lys	gly	ala	val	thr	pro	val	lys
					140				145						150
	asn	gln	gly	ser	cys	gly	ser	cys	trp	ala	phe	ser	ala	val	val

		155		160		165
	thr ile glu gly	ile ile lys ile arg	thr gly asn leu asn	glu		
		170		175		180
5	tyr ser glu gln	glu leu leu asp cys	asp arg arg ser tyr	gly		
		185		190		195
	cys asn gly gly	tyr pro trp ser ala	leu gln leu val ala	gln		
		200		205		210
	tyr gly ile his	tyr arg asn thr tyr	pro tyr glu gly val	gln		
		215		220		225
10	arg tyr cys arg	ser arg glu lys gly	pro tyr ala ala lys	thr		
		230		235		240
	asp gly val arg	gln val gln pro tyr	asn glu gly ala leu	leu		
		245		250		255
	tyr ser ile ala	asn gln pro val ser	val val leu glu ala	ala		
15		260		265		270
	gly lys asp phe	gln leu tyr arg gly	gly ile phe val gly	pro		
		275		280		285
	cys gly asn lys	val asp his ala val	ala ala val gly tyr	gly		
		290		295		300
20	pro asn tyr ile	leu ile lys asn ser	trp gly thr gly trp	gly		
		305		310		315
	glu asn gly tyr	ile arg ile lys arg	gly thr gly asn ser	tyr		
		320		325		330
25	gly val cys gly	leu tyr thr ser ser	phe tyr pro val lys	asn		
		335		340		345

## (2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
- 30 (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- 35 (iv) SOURCE ORIGIN:
- (A) ORGANISM: Plasmodium vinckei
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

40	phe pro asp ser arg	asp tyr arg ser lys	phe asn phe leu pro
		5	10
	pro lys asp gln gly	asn cys gly ser cys	trp ala phe ala ala
		20	25
	ile gly asn phe glu	tyr leu tyr val his	thr arg his glu met
45		35	40
	pro ile ser phe ser	glu gln gln met val	asp cys ser thr glu
		50	55
	asn tyr gly cys asp	gly gly asn pro phe	tyr ala phe leu tyr
		65	70
50	met ile asn asn gly	val cys leu gly asp	glu tyr pro tyr lys
		80	85
	gly his glu asp phe	phe cys leu asn tyr	arg cys ser leu leu
		95	100
	gly arg val his phe	ile gly asp val lys	pro asn glu leu ile
55		110	115
	met ala leu asn tyr	val gly pro val thr	ile ala val gly ala
		125	130
	ser glu asp phe val	leu tyr ser gly gly	val phe asp gly glu
		140	145
60	cys asn pro glu leu	asn his ser val leu	leu val gly tyr gly
		155	160
	gln val lys lys ser	leu ala phe glu asp	ser his ser asn val



		170		175		180
	asp ser asn leu	ile lys lys tyr lys	glu asn ile lys gly	asp		
		185		190		195
5	asp asp asp asp	ile ile tyr tyr trp	ile val arg asn ser	trp		
		200		205		210
	gly pro asn trp	gly glu gly gly tyr	ile arg ile lys arg	asn		
		215		220		225
	lys ala gly asp	asp gly phe cys gly	val gly ser asp val	phe		
		230		235		240
10	phe pro ile tyr					
		244				

## (2) INFORMATION FOR SEQ ID NO: 9:

## 15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## 20 (ii) MOLECULE TYPE: synthetic oligonucleotide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

AAAGGATCCT GC/TGGIA/TG/CITG C/TTGGGCITT 29

25

## (2) INFORMATION FOR SEQ ID NO: 10:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

## 30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: synthetic oligonucleotide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

35 TTTGAATTCC CAIG/CA/TA/GTTIC/T T/GIAC/TIATCCA A/GTA 33

## 40 (2) INFORMATION FOR SEQ ID NO: 11:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## 45 (ii) MOLECULE TYPE: synthetic oligonucleotide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CCAGGTACCA TGGACATAGG AAAC 24

50

## (2) INFORMATION FOR SEQ ID NO: 12:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

## 55 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: synthetic oligonucleotide

## (iv) ANTI- SENSE: YES

## 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CCCTCTAGAT GCTTATATTG ATTG

24

5

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

15 cys gly ser cys trp ala phe  
5 7

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: peptides

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

tyr trp ile val/ile lys/arg asn ser trp  
5 8

30

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

35 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

40 val arg asn ser trp  
5

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1203 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

50 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

55	ATGGACATAG	GAAACAACGT	GGAAGAACAT	CAGGAATATA	TTTCTGGACC	ATACATTGCA	60
	TTAATTAATG	GCACTAATCA	ACAAAGGGAA	CCGAATAAAA	AGTTGAAAAA	CATAATAATT	120
	GCAACGTTGA	TTGCAATCTT	TATAGTTTTG	GTTGTTACTG	TATCTTTGTA	TATTACTAAT	180
	AACACCAAGT	ACAAAATTGA	CGATTTCGTA	CCTGGTGATT	ATGTTGATCC	AGCAACTAGG	240
	GAGTATAGAA	AGAGTTTGA	GGAGTTCAAA	AAGAAATACC	ACAAAGTATA	TAGCTCTATG	300
	GAGGAGGAAA	ATCAAAGATT	TGAAATTTAT	AAGCAAAATA	TGAACTTTAT	TAAACAACA	360
60	AATAGCCAAG	GATTCAAGTA	TGTGTTAGAA	ATGAATGAAT	TTGGTGATTT	GTGCAAGAGAA	420
	GAGTTTATGG	CAAGATTCAC	AGGATATATA	AAAGATTCCA	AAGATGATGA	AAGGGTATTT	480
	AAGTCAAGTA	GAGTCTCAGC	AAGCGAATCA	GAAGAGGAAT	TTGTTCCCCC	AAATTCTATT	540

	AATTGGGTGG	AAGCTGGATG	CGTGAACCCA	ATAAGAAATC	AAAAGAATTG	TGGGTCATGT	600
	TGGGCTTTCT	CTGCTGTTGC	AGCTTTGGAG	GGAGCAACGT	GTGCTCAAAC	AAACCGAGGA	660
	TTACCAAGCT	TGAGTGAACA	GCAATTTGTT	GATTGCAGTA	AACAAAATGG	CAACTTTGGA	720
	TGTGATGGAG	GAACAATGGG	ATTGGCTTTT	CAGTATGCAA	TTAAGAACAA	ATATTTATGT	780
5	ACTAATGATG	ATTACCCTTA	CTTTGCTGAG	GAAAAAACAT	GTATGGATTG	ATTTTGCGAG	840
	AATTATATAG	AGATTCCTGT	AAAAGCCTAC	AAATATGTAT	TTCCGAGAAA	TATTAATGCA	900
	TTAAAGACTG	CTTTGGCTAA	GTATGGACCA	ATTTCAGTTG	CAATTCAGGC	CGATCAAACC	960
	CCTTTCCAGT	TTTATAAAAG	TGGAGTATTC	GATGCTCCTT	GTGGAACCAA	GGTTAATCAT	1020
	GGAGTTGTTT	TAGTTGAATA	TGATATGGAT	GAAGATACTA	ATAAAGAATA	TTGGCTAGTA	1080
10	AGAAATAGCT	GGGGTGAAGC	GTGGGGAGAG	AAAGGATACA	TCAAAC TAGC	TCTTCATTCT	1140
	GGAAAGAAGG	GAACATGTGG	TATATTGGTT	GAGCCAGTGT	ATCCAGTGAT	TAATCAATCA	1200
	ATA						1203